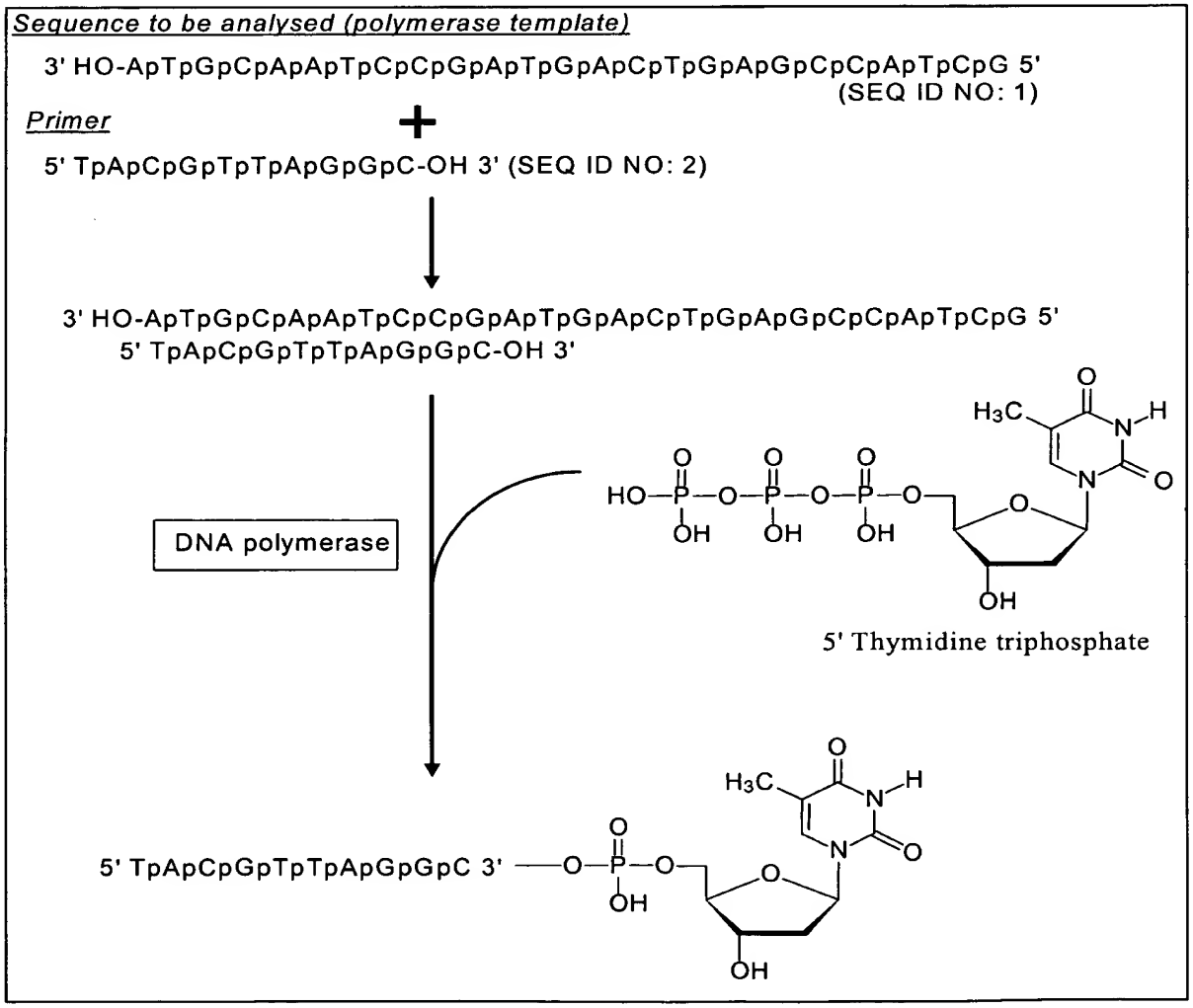
Amendments to the Specification:

Please delete the paragraph beginning on page 1 at line 18 with the words "The method most widely used" and extending through the end of Table 1 on page 2.

Please insert the following new paragraph beginning on page 1, line 18:

The method most widely used for analysing nucleic acid sequences is the enzymatic "chain termination" technique, developed by Sanger et al. in Proceedings of National Academy of Science, 74, 1977, p. 5463-5467 [1]. It is based on the properties of DNA-dependent DNA polymerases to create DNA polymers complementary to the sequence of a DNA strand serving as a template, from a mixture of natural nucleoside triphosphate monomers. The process consists, starting with the DNA strand to be analysed, in making a series of copies of the complementary strand by adding to the conventional reaction medium molecules known as "chain terminators" and then analysing the length of the newly formed strands to determine the base sequence of the template. The principle of the method is explained in Table 1 below.

Table 1

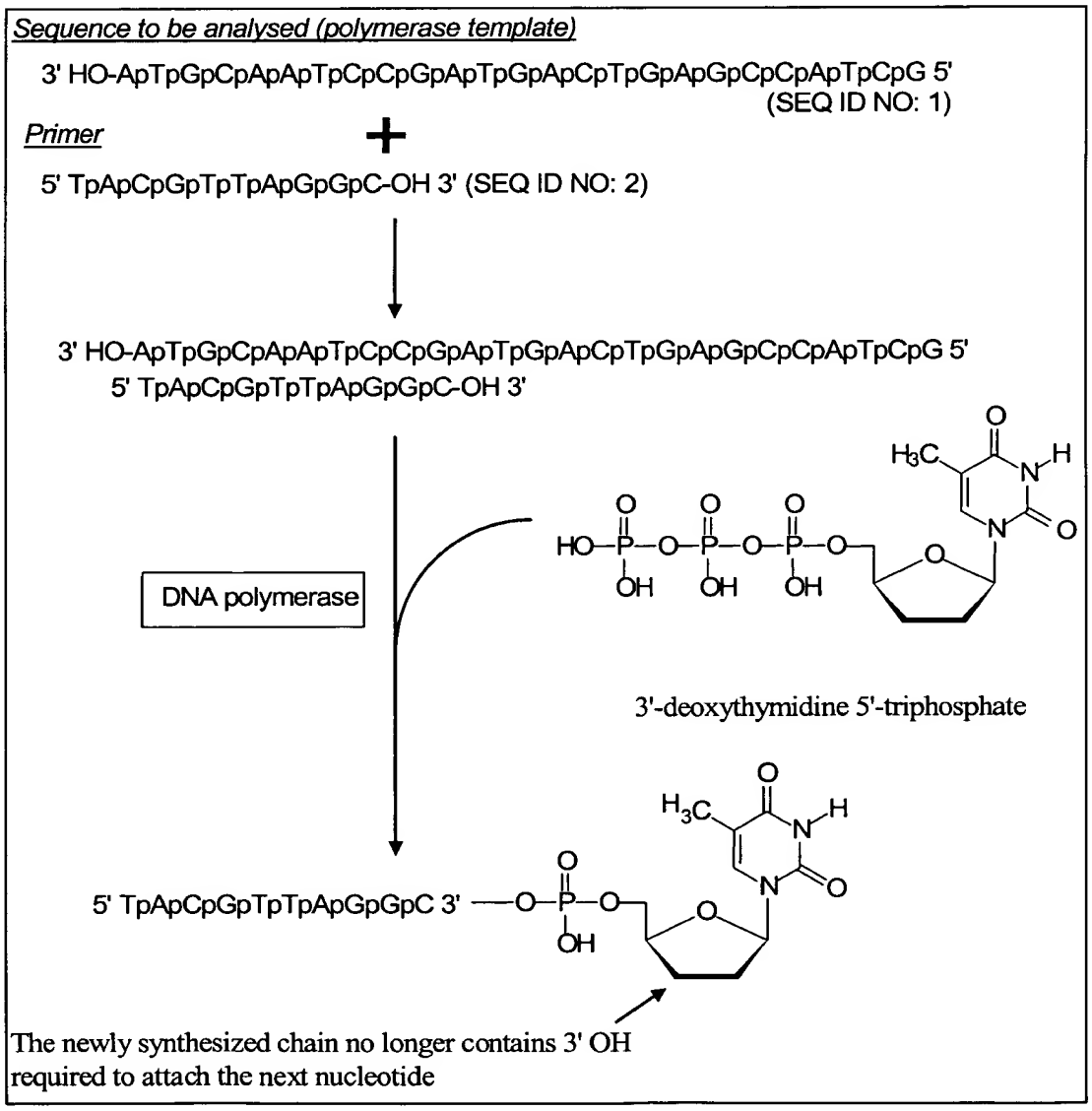


Please delete the paragraph beginning on page 3 at line 24 with the words "On the other hand" and extending through the end of Table 2 on page 4.

Please insert the following new paragraph beginning on page 3, line 24:

On the other hand, if a molecule which is recognized by the polymerase but which has no free 3'-OH terminal end is added to the reaction medium, each time this molecule is incorporated, the polymerization work of the enzyme will be interrupted because the chain can no longer grow on account of the absence of a site available to attach a new nucleotide (creation of interrupted newly-formed strands). This is illustrated in Table 2 below with 3'-deoxythymidine 5'-triphosphate.

Table 2



Please delete the paragraph beginning on page 4, line 6 with the words "Using this thymidine derivative" and extending through the end of Table 3 on page 5.

Please insert the following new paragraph beginning on page 4, line 6:

Using this thymidine derivative which will be referred to as a "T chain terminator" at a (inaudible) concentration, a series of DNA strands whose size is randomly fixed by the position of the adenines in the template is obtained for a given template. The result obtained is illustrated in Table 3. The sequence of the template is written in the first line and the sequence of the newly formed strands created with the T chain terminator (noted S) is written in the following lines.

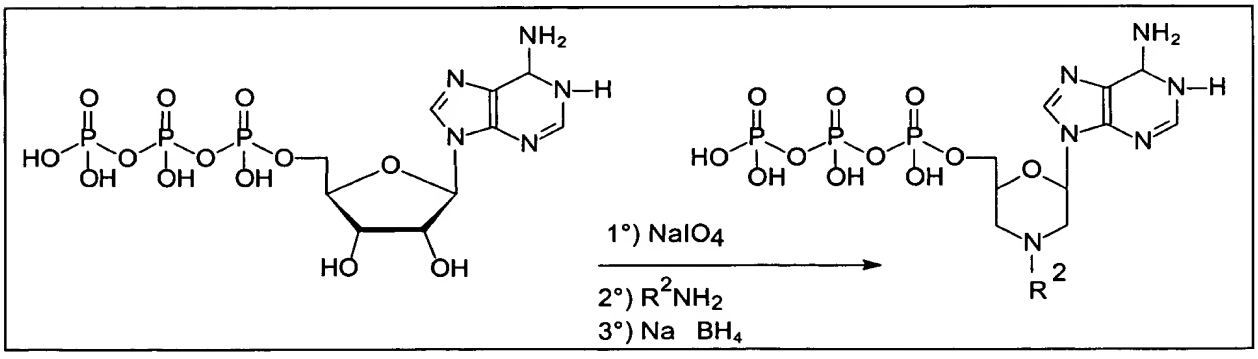
Table 3

TEMPLATE
3'- A T G C A T T C C G A C C T C T G A T C A G -5'
(SEQ ID NO: 3)
COPIES OF THE TEMPLATE
5'- **S**
5'- T A C G **S**
5'- T A C G T A A G G C **S** (SEQ ID NO: 4)
5'- T A C G T A A G G C T G G A G A C **S** (SEQ ID NO: 5)
5'- T A C G T A A G G C T G G A G A C T A G **S** (SEQ ID NO: 6)

Please delete the paragraph beginning on page 12 at line 14 with the words "The nucleotide derivatives" and extending through the reaction scheme.

Please insert the following new paragraph on page 12 beginning at line 14:

The nucleotide derivatives used in the process of the invention may be prepared in a single step, directly from ribonucleoside triphosphates, according to the following reaction scheme illustrated with R^1 representing adenine.



Please replace the paragraph beginning on page 47, line 10 with the following amended paragraph:

These two nucleoside triphosphate derivatives are tested in enzymatic incorporation to label an oligonucleotide 13 bases long at its 3' end. This labelling is referred to as "template-dependent" since the enzymes used need the complementary strand to extend the oligonucleotide according to the Watson & Crick rules. Sequence A (17870 pmol/mL) studied and also its complementary target C (16128 pmol/mL) are given in the figure below:

Target C:	3'-TGC CAA CCA ACC CCA CCT CAA CCT CTG-5' (SEQ ID NO: 7)
Primer A:	5'-ACG GTT GGT TGG G (13 bp) (SEQ ID NO: 8)
Expected fragments:	5'-ACG GTT TGG GGT GGA (18 bp) (SEQ ID NO: 9)
and lengths (bp) :	5'-ACG GTT GGT TGG GGT GGA GTT GGA (24 bp)(SEQ ID NO: 10)
	5'-ACG GTT GGT TGG GGT GGA GTT GGA GA (26 bp) (SEQ ID NO: 11)
	5'-ACG GTT GGT TGG GGT GGA GTT GGA GAC (27 bp) (SEQ ID NO: 12)

Please replace the paragraph beginning on page 53, line 5 with the following amended paragraph:

The solution B* thus contains 10 pmol of primer B in a volume of 50 µL. The solutions of C and B are also diluted tenfold; these solutions are noted, respectively, C/10 and B/10.

Target C :	3'-TGC CAA CCA ACC CCA CCT CAA CCT CTG-5' (SEQ ID NO: 7)
Primer B :	5'-ACG GTT GGT TGG GG (14 bp) (SEQ ID NO: 13)